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SEARCH REQUEST FORM

Date: 12/23/99 Requester's Full Name: Amy Nelson Examiner #: 73840
Art Unit: 1649 Phone (306) 3218 Serial Number: 09/327,230
Results Format Preferred (circle): PAPER DISK E-MAIL

****

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _____

Inventors (please provide full names): Gray et al.

_____

Earliest Priority Date: _____

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known.

For Sequence Searches Only *Please include all pertinent information (parent, grandchild, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search SEQ ID NO:1.

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_____ Other (specify)

****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 28 14:30:35 1999; MasPar time 5058.20 Seconds
1546.464 Million cell updates/sec

Tabular output not generated.

Title: >US-09-327-230-1
Description: (1-2822) from US09327230.seq
Perfect Score: 2822
N.A. Sequence: 1 gcaacgcacacagacaggca.....ttccaggtttgggtttcggg 2822
Comp: cgttgcgtgtgtctgtccgt.....aaggtccaaacccaaagccc

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 646147 seqs, 1385953633 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl58
1:em_ba1 2:em_ba2 3:em_fun 4:em_htg 5:em_hum1 6:em_hum2
7:em_in 8:em_om 9:em_or 10:em_ov 11:em_pat 12:em_ph
13:em_pl 14:em_ro 15:em_sts 16:em_vi
Database: genbank111
17:gb_ba1 18:gb_ba2 19:gb_htg1 20:gb_htg2 21:gb_in1
22:gb_in2 23:gb_om 24:gb_ov 25:gb_pat 26:gb_ph 27:gb_pl1
28:gb_pl2 29:gb_pr1 30:gb_pr2 31:gb_pr3 32:gb_ro
33:gb_st 34:gb_sts 35:gb_sy 36:gb_un 37:gb_vi

Statistics: Mean 12.024; Variance 6.432; scale 1.869

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
	1	2822	100.0	7129	28	ZMU77346	Zea mays lethal leaf-s	0.00e+00
	2	275	9.7	5364	28	AF050129	Zea mays cell wall inv	5.52e-180
c	3	83	2.9	7218	25	I66494	Sequence 14 from paten	3.13e-35
c	4	75	2.7	250	27	MZESUTZ82	Maize sucrose syntheta	1.13e-29
	5	59	2.1	7218	25	I66494	Sequence 14 from paten	6.69e-19
c	6	53	1.9	10772	21	AF012089	Drosophila melanogaste	5.10e-15
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c	8	45	1.6	250	27	MZESUTZ81	Maize sucrose syntheta	4.99e-10
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	10	43	1.5	6831	27	ZMA132240	Zea mays eIF-5 gene, e	8.02e-09
	11	39	1.4	965	25	AR024229	Sequence 22 from paten	1.81e-06
	12	38	1.3	1056	23	MVU87256	Mustela vison GT dinuc	6.78e-06
c	13	37	1.3	7905	27	MZECPN60B	Corn nuclear-encoded m	2.51e-05
	14	35	1.2	74371	31	AC005369	Homo sapiens chromosom	3.27e-04
	15	30	1.1	215	25	I28278	Sequence 5 from patent	1.48e-01
c	16	31	1.1	215	25	I28278	Sequence 5 from patent	4.54e-02
c	17	32	1.1	965	25	AR024229	Sequence 22 from paten	1.36e-02
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	19	31	1.1	216021	31	HUAC004787	Homo sapiens Chromosom	4.54e-02
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c	22	28	1.0	354	21	OFU89259	Oxytricha fallax 57kD	1.48e+00
c	23	27	1.0	364	27	MIECORI4	Yeast mitochondrial or	4.49e+00
	24	28	1.0	1663	23	MVU92534	Mustela vison microsat	1.48e+00
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	26	28	1.0	13594	22	AE001367	Plasmodium falciparum	1.48e+00
	27	28	1.0	29482	21	CEW05B5	Caenorhabditis elegans	1.48e+00
	28	27	1.0	36524	21	CELF33D4	Caenorhabditis elegans	4.49e+00
	29	28	1.0	42366	21	CEF25H2	Caenorhabditis elegans	1.48e+00
	30	29	1.0	55328	28	PWU02970	Prototheca wickerhamii	4.73e-01
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ALIGNMENTS

RESULT 1
LOCUS ZMU77346 7129 bp DNA PLN 15-APR-1997
DEFINITION Zea mays lethal leaf-spot 1 (lls1) gene, partial cds.
ACCESSION U77346
NID g1935910
VERSION U77346.1 GI:1935910
KEYWORDS .
SOURCE maize.
ORGANISM Zea mays
Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; vascular plants; seed plants; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
REFERENCE 1 (bases 1 to 7129)
AUTHORS Gray,J., Close,P.S., Briggs,S.P. and Johal,G.S.
TITLE A novel suppressor of cell death in plants encoded by the Lls1 gene of maize
JOURNAL Cell 89 (1), 25-31 (1997)
MEDLINE 97248483
REFERENCE 2 (bases 1 to 7129)
AUTHORS Gray,J. and Johal,G.S.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-1996) Agronomy, University of Missouri, 205 Curtis Hall, Columbia, MO 65211, USA
FEATURES Location/Qualifiers
source 1. .7129
/organism="Zea mays"
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/db_xref="taxon:4577"
/chromosome="1S"
/map="Bin 1.01 - 1.03"
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/product="unknown"
/protein_id="AAC49677.1"
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                     /number=1
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                     /note="encodes proline-cysteine motif suggested to be
                     important in coordinating the [4Fe-4S] iron-sulfur center"
     intron          3765. .3853
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                     /number=1
     exon            3854. .4089
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     intron          4305. .5479
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                     /number=3
     exon            5480. .5616
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ORIGIN

  Query Match          100.0%;  Score 2822;  DB 28;  Length 7129;
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Db    353 CTATTCGTCTTAAGTTTTTTTGTTCAACATCACATACTTGTGTTGCTAATGTAACAAAAA 412
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Db    413 AAATTCACACGCCTCACAAACATTACAATATGATTCAAAATAGACACTAACCAAACCTTG 472
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Qy    121 aaattcacacgcctcacaaacattacaatatgattcaaaatagacactaaccaaaccttg 180

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Db    533 AGGAAATACACACGAGCAACTGTTGTGGACTTGTTGCAAAATAGCAAGGAAAGGTATTAG 592
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Db   2213 CTTATAATGGTTACTATAGGTTGAGGGACGGAAGTAGTAGTAGAACTGGTAAACAAATTC 2272
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Db   2393 CCCTCCGCGCGGCGCAATTCGTCCCGGTGGGGACGGCTAGCTGGCCCAATGCCAAAGCTC 2452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2101 ccctccgcgcggcgcaattcgtcccggtggggacggctagctggcccaatgccaaagctc 2160

Db   2453 CACCGACAAATGCCGCAAAGCGCCATGCGTGGTCGCGTACAATTGCCTCCTTCCCCGCCC 2512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2161 caccgacaaatgccgcaaagcgccatgcgtggtcgcgtacaattgcctccttccccgccc 2220

Db   2513 TTCCTCCCTTCCCTGCCGTGACGCAACCACACTGCGCTCACCATCGTGTACAATGTATTC 2572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2221 ttcctcccttccctgccgtgacgcaaccacactgcgctcaccatcgtgtacaatgtattc 2280

Db   2573 TCCCTAGCCGAACCGTATCAGTAGTTCTTAGGGGTGGGCGTTCGGGTTACCCGAAATTTT 2632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2281 tccctagccgaaccgtatcagtagttcttaggggtgggcgttcgggttacccgaaatttt 2340

Db   2633 CGGGTTGGGTAATTCAAGTTTTTTAAATTTCGGGTTTTGAGAATCAATACCCGAAATTAC 2692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2341 cgggttgggtaattcaagtttttaaatttcgggttttgagaatcaatacccgaaattac 2400

Db   2693 AACGGATTTTTCAATACCCGGAATTTCGGGTACCCGGAATTTCGGGTTCGGGTTCGGGTA 2752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2401 aacggatttttcaatacccggaatttcgggtacccggaatttcgggttcgggttcgggta 2460

Db   2753 TTCCCAAACTACCCGAACTATTGTGTTGGCTTCATAAAAACACATACACCCTATTAAATT 2812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2461 ttcccaaactacccgaactattgtgttggcttcataaaaacacatacaccctattaaatt 2520

Db   2813 AGTATAAAAATATAGTTTGAATAATGATATACATGGACATATAAAACACAAACAATCTAC 2872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2521 agtataaaaatatagtttgaataatgatatacatggacatataaaacacaaacaatctac 2580

Db   2873 AATCCCAAGTTATGCACACTTACACATAATTATAGATGTACAAACTTAAATTATTAAAGC 2932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2581 aatcccaagttatgcacacttacacataattatagatgtacaaacttaaattattaaagc 2640

Db   2933 ATGACATGAGTACATGACACATGAAAGCCGGGTAATTCGGGTATTTCGGGTACCCGATTG 2992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2641 atgacatgagtacatgacacatgaaagccgggtaattcgggtatttcgggtacccgattg 2700

Db   2993 TGATACCCGAATTACCCGAAATAATTTCGGGTTTTGCAAGTTGCTACCCGAAATTCCCAA 3052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2701 tgatacccgaattacccgaaataatttcgggttttgcaagttgctacccgaaattcccaa 2760

Db   3053 ACAAAATTCGGGTTTCGGGTATTTCGGGTTCGGGTTCGGGTATTCCAGGTTTGGGTTTCG 3112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2761 acaaaattcgggtttcgggtatttcgggttcgggttcgggtattccaggtttgggtttcg 2820

Db   3113 GG 3114
          ||
Qy   2821 gg 2822
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```
RESULT    2
LOCUS       AF050129     5364 bp    DNA             PLN       02-JAN-1999
DEFINITION  Zea mays cell wall invertase Incw1 gene, complete cds.
ACCESSION   AF050129
NID         g4105720
VERSION     AF050129.1  GI:4105720
KEYWORDS    .
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
            Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
            Poales; Poaceae; Zea.
REFERENCE   1  (bases 1 to 5364)
  AUTHORS   Kim,J.Y., Mahe,A., Guy,S., Brangeon,J., Roche,O., Chourey,P.S. and
            Prioul,J.L.
  TITLE     Molecular cloning, characterization and expression of two maize
            genes encoding cell wall invertase (Incw3 and Incw4)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 5364)
  AUTHORS   Taliercio,E.W., Kim,J.Y., Mahe,A., Shanker,S., Choi,J., Cheng,W.H.,
            Prioul,J.L. and Chourey,P.S.
  TITLE     Isolation, characterization and expression analyses of two cell
            wall invertase genes in maize (Incw1 and Incw2)
```

```
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 5364)
  AUTHORS   Kim,J.Y., Mahe,A., Taliercio,E.W., Chourey,P.S. and Prioul,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-FEB-1998) Institut de Biotechnologie des Plantes,
            CNRS-ERS 569, Universite Paris-Sud (XI), Bat 630, Orsay 91405,
            France
FEATURES             Location/Qualifiers
     source          1. .5364
                     /organism="Zea mays"
                     /strain="W22"
                     /db_xref="taxon:4577"
                     /chromosome="5"
                     /map="between gsy60e (bt2) and bnl771"
     mRNA            join(<1. .208,821. .829,1441. .2306,2548. .2706,3253. .3509,
                     3636. .3726,3818. .>4003)
                     /product="cell wall invertase Incw1"
     CDS             join(1. .208,821. .829,1441. .2306,2548. .2706,3253. .3509,
                     3636. .3726,3818. .4003)
                     /EC_number="3.2.1.26"
                     /function="sucrose hydrolysis"
                     /note="beta-fructosidase"
                     /codon_start=1
                     /product="cell wall invertase Incw1"
                     /protein_id="AAD02511.1"
                     /db_xref="PID:g4105721"
                     /db_xref="GI:4105721"
                     /translation="MGTRPRGVVLAPWAVVLVLVLVLALRLAGASHVIHRSLEAEVPP
                     SVPASIVSPLLRTGYHFQPPMNWINDPNAPLYYKGWYHLFYQYNPKGAVWGNIVWAHS
                     VSRDLINWVALEAAIYPSIPSDKYGCWSGSATILEDGTPAILYTGIDRPDINYQVQVL
                     ALPKDASDPLLREWEKPEEYNPVATPAAGINATQFRDPTTAWRHAGAGHWRMLVGSVR
                     GARGMALVYRSRDFRTWTKAKHPLHSAALTGMWECPDFFPVSGPGLQAGLDTSAPGTK
                     YVLKSSLDLTRYDYYTIGSYDGGKDRYYPDDPAGDYRRRLRYDYGNYYASKTFYDPVE
                     RRRVLLGWANESDSVPDDKAKGWAGIHAIPRKIWLDPTGKQLLQWPIHEVEKLRGKAV
                     SVDAKLVKPGDHFEVTGIATYQADVEVSFELEAGTSLLEKAEAFDPAYDDDAQKLCGV
                     KGADARGGVGPFGLWVLASADLQERTAVFFRVFRDGHGKPKVLMCTDPTKSSLSPDLY
                     KPTLAGLVDADISSGKITLRSLIDRSVVESFGAGGKTCILSRVYPSIAVGKDAHLYVF
                     NNGEVDVTVSGLTAWEMKKPLMNGA"
     polyA_signal    4296. .4301
BASE COUNT     1255 a   1352 c   1403 g   1354 t
ORIGIN

  Query Match             9.7%;  Score 275;  DB 28;  Length 5364;
  Best Local Similarity  92.8%;  Pred. No. 5.52e-180;
  Matches   298;  Conservative    0;  Mismatches  23;  Indels   0;  Gaps   0;

Db    5043 GTGCCTAGGGGTGGGCGTTCGGATTACCCGAAAATTTCGGGTCGGGTATTTCGGGTTTTT 5102
           || | |||||||||||||||||| |||||||||| |||||||| ||||| |||  ||||||
Qy    2304 gttcttaggggtgggcgttcgggttacccgaaattttcgggttgggtaattcaagttttt 2363

Db    5103 AAAATTTTGGGTTTTGAGAATCGCTACCCGAAATTACAACGGGTTTTGCAATACCCGAAA 5162
           ||||||  |||||||||||||||  ||||||||||||||||||| |||| |||||||||  ||
Qy    2364 taaatttcgggttttgagaatcaatacccgaaattacaacggatttttcaatacccggaa 2423

Db    5163 ATTCGGGTACCCAGAATTTCGGGTTCGGGTTCGGGTATTCCCGAACTACCCGAACTATTA 5222
           ||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Qy    2424 tttcgggtacccggaatttcgggttcgggttcgggtattcccaaactacccgaactattg 2483

Db    5223 TGTCGGCTTCATAAAAACACATACACCCTATTAAATTAGTATAAAAATATAGTTTGAATA 5282
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    2484 tgttggcttcataaaaacacatacaccctattaaattagtataaaaatatagtttgaata 2543

Db    5283 ATGATATACATGGACATATAAAACACAATCAATCTACAATCACAAGTTATGCACACTTAC 5342
           |||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||
Qy    2544 atgatatacatggacatataaaacacaaacaatctacaatcccaagttatgcacacttac 2603

Db    5343 ACATAATTATAGATGCACAAA 5363
           |||||||||||||| |||||
Qy    2604 acataattatagatgtacaaa 2624


RESULT    3
LOCUS       I66494       7218 bp    DNA             PAT       23-DEC-1997
DEFINITION  Sequence 14 from patent US 5670367.
ACCESSION   I66494
NID         g2724471
VERSION     I66494.1  GI:2724471
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7218)
  AUTHORS   Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
  TITLE     Recombinant fowlpox virus
  JOURNAL   Patent: US 5670367-A 14 23-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .7218
                     /organism="unknown"
BASE COUNT     1944 a   1491 c   1486 g   1929 t    368 others
ORIGIN

  Query Match             2.9%;  Score 83;  DB 25;  Length 7218;
  Best Local Similarity   0.8%;  Pred. No. 3.13e-35;
  Matches     3;  Conservative  219;  Mismatches 139;  Indels   0;  Gaps   0;

Db    1064 GATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1123
           |||:::::: :::::    :::  :     :  ::::  ::  : : :: : :: : : :
Cp     594 gatttccttatctttaaagcccgacggaaacggccccaactagcatatcatgccgtgcat 535

Db    1124 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1183
            : :::   :::::: : :::  :: ::::    : :::  :: :: : :: :: ::::
Cp     534 gcgttcgagcccttcatatctgaccattttggaacatttagttattgtgttgctgccctc 475

Db    1184 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1243
             ::  :: :::::: ::::: :  ::   :::::::: :::  :  ::: ::   :::
Cp     474 gtcagtcattctttgtccttgtaattgaattcttttcaatccaatagtctgctagattta 415

Db    1244 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1303
           : :  : : : :: ::: :::: ::: : :  :::::: :::: : : : :    : ::
Cp     414 cataacgcatgttgttcactttacctatatagtttttttatttcatacatgtaaggtacta 355

Db    1304 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1363
                :  :: :: :: :: : ::: :  ::::: :  :: : ::: :: :: ::  :
Cp     354 aagagcagactatcattgttatacttgcagctcctacaattatgcttgctattactaata 295

Db    1364 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1423
           ::::::::: :: :::: :  :   ::: :  :  :: ::: : : : :::::::: :::
Cp     294 cctttccttgctattttgcaacaagtccacaacagttgctcgtgtgtatttcctctgtct 235

Db    1424 Y 1424
           :
Cp     234 c 234


RESULT    4
LOCUS       MZESUTZ82     250 bp    DNA             PLN       08-MAY-1993
DEFINITION  Maize sucrose synthetase gene mutant (Sh-5586 allele), containing
            transposon Tz86, 3' end of Tz86.
ACCESSION   M10175
NID         g168630
VERSION     M10175.1  GI:168630
KEYWORDS    sucrose synthase 3; transposon.
SEGMENT     2 of 2
SOURCE      Z. mays DNA.
  ORGANISM  Zea mays
            Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
            Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
            Liliopsida; Poales; Poaceae; Zea.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Dellaporta,S.L., Chomet,P.S., Mottinger,J.P., Wood,J.A., Yu,S.M.
            and Hicks,J.B.
  TITLE     Endogenous transposable elements associated with virus infection in
            maize
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 49, 321-328 (1984)
  MEDLINE   85153004
COMMENT     See segment 1.
```

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FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Zea mays"
                     /db_xref="taxon:4577"
     repeat_region   231. .240
                     /note="10 bp duplication"
BASE COUNT       69 a     57 c     54 g     70 t
ORIGIN      About 3.4 kb after segment 1.

  Query Match             2.7%;  Score 75;  DB 27;  Length 250;
  Best Local Similarity  77.4%;  Pred. No. 1.13e-29;
  Matches   127;  Conservative    0;  Mismatches  34;  Indels   3;  Gaps   3;

Db     64 TCGGGTAGAACGGGC-TACCCGAACCCGAACCCGAATTTTTTGGGTACCCGAATTTTCGG 122
          ||||||||   |||  ||||||||||||||||||||| ||   |||||||||||| || |||
Cp   2476 tcgggtagtttgggaatacccgaacccgaacccgaaattcc-gggtacccgaaattccgg 2418

Db    123 GTTTTGCTTAAATTGGGTACATATTCGGGTATTGTTTCTGAAAACCCGAATTGTTAAAAG 182
          || |||   ||||  | |  |  |||||||||| |||| |||||||||| | | ||||
Cp   2417 gtattgaa-aaatccgttgtaatttcgggtattgattctcaaaacccgaaatttaaaaaa 2359

Db    183 CCCAAACTACCCGACCCGAAAATTCGGGCTAACCCGAATGCCCA 226
          |   || ||||| ||||||||||  || |||||||| |||||
Cp   2358 cttgaattacccaacccgaaaatttcgggtaacccgaacgccca 2315


RESULT    5
LOCUS       I66494       7218 bp    DNA             PAT       23-DEC-1997
DEFINITION  Sequence 14 from patent US 5670367.
ACCESSION   I66494
NID         g2724471
VERSION     I66494.1  GI:2724471
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7218)
  AUTHORS   Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
  TITLE     Recombinant fowlpox virus
  JOURNAL   Patent: US 5670367-A 14 23-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .7218
                     /organism="unknown"
BASE COUNT     1944 a   1491 c   1486 g   1929 t    368 others
ORIGIN

  Query Match             2.1%;  Score 59;  DB 25;  Length 7218;
  Best Local Similarity   1.6%;  Pred. No. 6.69e-19;
  Matches     6;  Conservative  211;  Mismatches 158;  Indels   0;  Gaps   0;

Db   1066 TYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1125
          |:::   ::::::  :  ::::::::::::::::: : :: : : ::   : :: :::::
Qy   1060 ttttgagcctcccaacagtccccttcccctcccccatattacgcgtcaagcattgttccc 1119

Db   1126 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1185
             :: :::::: : : : ::  ::::: : : : :::::::: : : :  :::: ::
Qy   1120 aatcgtcctctgcgcatgctggttcccacgtgtattttcctcgcgcgcagttctgttgga 1179

Db   1186 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1245
                   :    : ::  : ::  : ::  ::     :: :  :: :: :  ::  ::
Qy   1180 ggaggaaggcgggacgttggcactagcgctggctggagattatggccatcgcaatcagtt 1239

Db   1246 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1305
          : :  :  ::   : :::: :::::::  :: ::: : :   :  : :: ::::: :     :
Qy   1240 tgtggcagtcaaatgctttgttttttggccgctcatgtgagtatcatttctgtgaaaac 1299

Db   1306 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1365
          : :::   ::  : :   : : : :::::::   :: :: :  :       :::: :: :
Qy   1300 tatctaaatcaatatgaatgtatatttctttaagtcgtcacgataggaagactccatcgt 1359

Db   1366 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1425
          :::    :::   :: : : : : : ::: :::::::::   : :   :::: :  : ::
Qy   1360 tctaaaacctaaaccatgcacacatattcatctttctccaaacgcaagtctcgtgatatt 1419

Db   1426 YYYYYYYYYGTACCA 1440
          : : ::::::|| |||
Qy   1420 tatattctcgtgcca 1434


RESULT    6
LOCUS       AF012089    10772 bp    DNA             INV       05-AUG-1997
DEFINITION  Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete
            cds, and phenylalanyl tRNA synthetase gene, partial cds.
ACCESSION   AF012089
NID         g2305220
VERSION     AF012089.1  GI:2305220
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
            Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 4546 to 4553)
  AUTHORS   Gray,Y.H., Tanaka,M.M. and Sved,J.A.
  TITLE     P-element-induced recombination in Drosophila melanogaster: hybrid
            element insertion
  JOURNAL   Genetics 144 (4), 1601-1610 (1996)
  MEDLINE   97132596
REFERENCE   2  (bases 1 to 10772)
  AUTHORS   Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
  TITLE     Structure of the cysteine proteinase (CP1) gene of Drosophila
            melanogaster and associated mutational effects
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 10772)
  AUTHORS   Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-1997) School of Biological Sciences, University
            of Sydney, Biology A12, Sydney University, NSW 2006, Australia
FEATURES             Location/Qualifiers
     source          1. .10772
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
     mRNA            join(872. .1000,2310. .2426,6476. .6690,6751. .7707)
                     /gene="CP1"
                     /product="cysteine protease"
     gene            872. .7707
                     /gene="CP1"
     exon            872. .1000
                     /gene="CP1"
                     /number=1
     intron          1001. .2309
                     /gene="CP1"
     exon            2310. .2426
                     /gene="CP1"
                     /number=2
     CDS             join(2328. .2426,6476. .6690,6751. .7462)
                     /gene="CP1"
                     /codon_start=1
                     /product="cysteine proteinase-1"
                     /protein_id="AAB65749.1"
                     /db_xref="PID:g2305221"
                     /db_xref="GI:2305221"
                     /translation="MRTAVLLPLLALLAVAQAVSFADVVMEEWHTFKLEHRKNYQDET
                     EERFRLKIFNENKHKIAKHNQRFAEGKVSFKLAVNKYADLLHHEFRQLMNGFNYTLHK
                     QLRAADESFKGVTFISPAHVTLPKSVDWRTKGAVTAVKDQGHCGSCWAFSSTGALEGQ
                     HFRKSGVLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
                     DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
                     EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
                     ASSYPLV"
     intron          2427. .6475
                     /gene="CP1"
     misc_feature    4546. .4553
                     /gene="CP1"
                     /note="insertion site of P{CaSpeR}(50C)"
                     /citation=[1]
     exon            6476. .6690
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                     /gene="CP1"
                     /number=3
     intron          6691. .6750
                     /gene="CP1"
     exon            6751. .7707
                     /gene="CP1"
                     /number=4
     mRNA            join(<8110. .9300,9370. .>9532)
                     /product="phenylalanyl tRNA synthetase"
     CDS             join(8110. .9300,9370. .>9532)
                     /note="potential orf"
                     /codon_start=1
                     /product="phenylalanyl tRNA synthetase"
                     /protein_id="AAB65750.1"
                     /db_xref="PID:g2305222"
                     /db_xref="GI:2305222"
                     /translation="MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
                     TDGWTNVTPKILSYVGANKHLQTDHPLSIIRQRIVNYFYGAYRNQRGNPLFSVYDQMN
                     PVVTVQQNFDNLLIPADHVSRQKSDCYYINQQHLLRAHTTAHQVELISGGLDNFLVVG
                     EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLELFEETWSGTLADPKLILPHP
                     SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
                     YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
                     GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
                     DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
                     IX"
BASE COUNT     2929 a   2357 c   2282 g   3046 t    158 others
ORIGIN

  Query Match            1.9%;  Score 53;  DB 21;  Length 10772;
  Best Local Similarity  21.2%;  Pred. No. 5.10e-15;
  Matches    29;  Conservative   71;  Mismatches  35;  Indels   2;  Gaps   2;

Db   1694 WWYWAWTTTMWKWMWTTWKWAMMKTYRTWWMWKMYWTSRTTTTSAMWMWYTWSTWTKYWW 1753
            :: :|:| |:::: :||::: : :|::|:::: :::|::| |   : :: |::|:|: ::
Cp    883 taaaaatataagattttatatattttattaaacctatcatgtatcagaagtacttttat 825

Db   1754 AYAWMKMWWTRTWARMAWASWARWKWKTSAAAAYSAWRKMWKWWAYRAMKKTWMWAAWKW 1813
           |:|  :  : :  |   :| :|:::::|:    ::|:: ::: :| : :::|:::||: :
Cp    824 atagttggtcaagattttaaaagatagtgctcttcaaa-aagcaagacattttaaaaaat 766

Db   1814 RWKAAWWTWRWWYMTTT 1830
           :   |::|::::: |||
Cp    765 ggagatatagtacttttt 749


RESULT    7
LOCUS       AF012089    10772 bp    DNA             INV       05-AUG-1997
DEFINITION  Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete
            cds, and phenylalanyl tRNA synthetase gene, partial cds.
ACCESSION   AF012089
NID         g2305220
VERSION     AF012089.1  GI:2305220
KEYWORDS    .
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
            Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 4546 to 4553)
  AUTHORS   Gray,Y.H., Tanaka,M.M. and Sved,J.A.
  TITLE     P-element-induced recombination in Drosophila melanogaster: hybrid
            element insertion
  JOURNAL   Genetics 144 (4), 1601-1610 (1996)
  MEDLINE   97132596
REFERENCE   2  (bases 1 to 10772)
  AUTHORS   Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
  TITLE     Structure of the cysteine proteinase (CP1) gene of Drosophila
            melanogaster and associated mutational effects
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 10772)
  AUTHORS   Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-1997) School of Biological Sciences, University
            of Sydney, Biology A12, Sydney University, NSW 2006, Australia
FEATURES             Location/Qualifiers
     source          1. .10772
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
     mRNA            join(872. .1000,2310. .2426,6476. .6690,6751. .7707)
                     /gene="CP1"
                     /product="cysteine protease"
     gene            872. .7707
                     /gene="CP1"
     exon            872. .1000
                     /gene="CP1"
                     /number=1
     intron          1001. .2309
                     /gene="CP1"
     exon            2310. .2426
                     /gene="CP1"
                     /number=2
     CDS             join(2328. .2426,6476. .6690,6751. .7462)
                     /gene="CP1"
                     /codon_start=1
                     /product="cysteine proteinase-1"
                     /protein_id="AAB65749.1"
                     /db_xref="PID:g2305221"
                     /db_xref="GI:2305221"
                     /translation="MRTAVLLPLLALLAVAQAVSFADVVMEEWHTFKLEHRKNYQDET
                     EERFRLKIFNENKHKIAKHNQRFAEGKVSFKLAVNKYADLLHHEFRQLMNGFNYTLHK
                     QLRAADESFKGVTFISPAHVTLPKSVDWRTKGAVTAVKDQGHCGSCWAFSSTGALEGQ
                     HFRKSGVLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
                     DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
                     EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
                     ASSYPLV"
     intron          2427. .6475
                     /gene="CP1"
     misc_feature    4546. .4553
                     /gene="CP1"
                     /note="insertion site of P{CaSpeR}(50C)"
                     /citation=[1]
     exon            6476. .6690
                     /gene="CP1"
                     /number=3
     intron          6691. .6750
                     /gene="CP1"
     exon            6751. .7707
                     /gene="CP1"
                     /number=4
     mRNA            join(<8110. .9300,9370. .>9532)
                     /product="phenylalanyl tRNA synthetase"
     CDS             join(8110. .9300,9370. .>9532)
                     /note="potential orf"
                     /codon_start=1
                     /product="phenylalanyl tRNA synthetase"
                     /protein_id="AAB65750.1"
                     /db_xref="PID:g2305222"
                     /db_xref="GI:2305222"
                     /translation="MLLTLRVQGARHWLKSTRCLASSAAPAKSPSSPPQLEVSGSTYA
                     TDGWTNVTPKILSYVGANKHLQTDHPLSIIRQRIVNYFYGAYRNQRGNPLFSVYDQMN
                     PVVTVQQNFDNLLIPADHVSRQKSDCYYINQQHLLRAHTTAHQVELISGGLDNFLVVG
                     EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLELFEETWSGTLADPKLILPHP
                     SSWTKPNSPATRRAVKLMEHEMKHVLVGLTKDLFGPRIKYRWVDTYFPFTQPSWELEI
                     YFKDNWLEVLGCGIMRHEILQRSGVHQSIGYAFGVGLERLAMVLFDIPDIRLFWSNDS
                     GFLSQFSEKDLHNLPKYKPISHYPQCTNDLSFWLPQDIEVDAGFSPNDFYDLVRSVAG
                     DMVEQISLVDKFKHPKTGKSSVCFRIVYRHMERTLTQAEVNEIHKQIASASVDSFNVQ
                     IX"
BASE COUNT     2929 a   2357 c   2282 g   3046 t    158 others
ORIGIN

  Query Match            1.7%;  Score 49;  DB 21;  Length 10772;
  Best Local Similarity  19.0%;  Pred. No. 1.71e-12;
  Matches    26;  Conservative   72;  Mismatches  37;  Indels   2;  Gaps   2;

Db   1689 AAAKRWWYWAWTTTMWKWMWTTWKWAMMKTYRTWWMWKMYWTSRTTTTSAMWMWYTWSTW 1748
           ||| :::::|: |    : :||:::|::: : |: ::: ::|::    :|::::|: |:
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Qy     749 aaaagtactatatctccatttttttaaaatgtcttgctt-tttgaagagcactatctttta 807

Db    1749 TKYWWAYAWMKMWWTRTWARMAWASWARWKWKTSAAAAYSAWRKMWKWWAYRAMKKTWMW 1808
           :  : :: :: |:|: ::|: ::| :: :   | |::|::: ::::|::|: : :::
Qy     808 aaatcttgaccaactatataaaa-gtacttctgatacatgataggtttaataaaatatat 866

Db    1809 AAWKWRWKAAWWTWRWW 1825
           ||: : ::| ::|: ::
Qy     867 aaaatcttatatttttta 883


RESULT    8
LOCUS       MZESUTZ81     250 bp    DNA             PLN       08-MAY-1993
DEFINITION  Maize sucrose synthetase gene mutant (Sh-5586 allele) containing
            transposon Tz86, 5' end of Tz86.
ACCESSION   M10174
NID         g168629
VERSION     M10174.1  GI:168629
KEYWORDS    sucrose synthase 3; transposon.
SEGMENT     1 of 2
SOURCE      Z. mays DNA.
  ORGANISM  Zea mays
            Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
            Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
            Liliopsida; Poales; Poaceae; Zea.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Dellaporta,S.L., Chomet,P.S., Mottinger,J.P., Wood,J.A., Yu,S.M.
            and Hicks,J.B.
  TITLE     Endogenous transposable elements associated with virus infection in
            maize
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 49, 321-328 (1984)
  MEDLINE   85153004
COMMENT     The transposon Tz86 generates a 10 bp duplication of target
            sequence upon integration.  This sucrose synthetase allele (with
            the Tz86 insertion) been named sh-5586.  [1] estimates Tz86 to be
            3.6 kb in length.
FEATURES             Location/Qualifiers
     source          1. .250
                     /organism="Zea mays"
                     /db_xref="taxon:4577"
     CDS             <1. .41
                     /note="sucrose synthetase,  (putative); putative"
                     /codon_start=3
                     /number=15
                     /protein_id="AAA33516.1"
                     /db_xref="PID:g168632"
                     /db_xref="GI:168632"
                     /translation="ASRYTGSSTPRG"
     repeat_region   34. .43
                     /note="10 bp duplication"
BASE COUNT       84 a     74 c     49 g     43 t
ORIGIN      1 bp upstream of HindIII site.

  Query Match           1.6%;  Score 45;  DB 27;  Length 250;
  Best Local Similarity  69.8%;  Pred. No. 4.99e-10;
  Matches    97;  Conservative    0;  Mismatches  40;  Indels   2;  Gaps   2;

Db      78 AAACCCGAAAAACCCGAGCCCGAACCCGTATAGCCCAATACCCGATACCCGAAATATTTA 137
           ||||| | || |||||| |||||||||| |   ||| | ||||||     |
Cp    2812 aaacctggaataccgaacccgaacccgaaatacccgaaacccgaatttttgtttgggaat 2753

Db     138 TGCGGGCAGTAAACCTTAAAACCCGATATTATTTCGGGCTTAATCGGGTAGCAACACCGG 197
           | |||| || ||     |||||||| |||||||||| | | ||||||| ||  | |||
Cp    2752 ttcgggtagcaacttgcaaaacccgaaattatttcggg-taattcgggtatcacaatcgg 2694

Db     198 -TACCCGAAATACCCAAAT 215
            ||||||||||||||| |||
Cp    2693 gtacccgaaatacccgaat 2675


RESULT    9
LOCUS       ZMCI31AC3     5057 bp    DNA             PLN       24-FEB-1999
DEFINITION  Z.mays cyp71c3 gene.
ACCESSION   Y11403
NID         g1870202
VERSION     Y11403.1  GI:1870202
KEYWORDS    CYP71C3 gene; Cytochrome P450.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
            Poaceae; Zea.
REFERENCE   1  (bases 1 to 5057)
  AUTHORS   Gierl,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-1997) A. Gierl, TU-Muenchen, Genetic,
            Lichtenbergstrasse 4, 85747 Garching, FRG
REFERENCE   2  (bases 1 to 5057)
  AUTHORS   Frey,M., Chomet,P., Glawischnig,E., Stettner,C., Grun,S.,
            Winklmair,A., Eisenreich,W., Bacher,A., Meeley,R.B., Briggs,S.P.,
            Simcox,K. and Gierl,A.
  TITLE     Analysis of a chemical plant defense mechanism in grasses
  JOURNAL   Science 277 (5326), 696-699 (1997)
  MEDLINE   97382314
FEATURES             Location/Qualifiers
     source          1. .5057
                     /organism="Zea mays"
                     /cultivar="ci31a"
                     /db_xref="taxon:4577"
                     /chromosome="4"
                     /dev_stage="seedling"
     exon            2171. .2736
                     /number=1
     gene            2203. .4029
                     /gene="cyp71c3"
     CDS             join(2203. .2736,2833. .3273,3397. .4029)
                     /gene="cyp71c3"
                     /codon_start=1
                     /product="cytochrome p450"
                     /protein_id="CAA72207.1"
                     /db_xref="PID:e304532"
                     /db_xref="PID:g1870203"
                     /db_xref="GI:1870203"
                     /db_xref="SWISS-PROT:P93703"
                     /translation="MALQAAYEYLQQAVGHGAWSSTQTLTLLLIAVPTVLLLLASLAK
                     STSSSGRGKPPLPPSPPGTLPIVGHLHHIGPQTHISLQELVAKYGHNGFLFLRAGAVP
                     TLIVSSPSAAEAVMRTHDHICASRPWSMASHILRYNTCDVAFSPLGEYWQQTRKLMNT
                     HLLSNKKVYSFRHGREEEVCLVVDNLREAAAKSPSTAVDMSEVLAAYTNDVVSRSVLG
                     STHRKKGRNTLFREMTMTNVDLLVGFNLEYYIPRWPLTDLLFRLVCWKVTRHLKRWDA
                     LLEEVIHEHVEMRKLSGDKEKESDDFIDIFLSRYEEYGFTMDNVKSLLMNVFEAAIET
                     SYLVLESAMAELMNHRRVMKKLQAEVRAYGAEKKLDMIREDDLSSLPYLKASMKEALR
                     LHPPGPLLLPHYSTADCQIDGYHIPANPRVLVNGWAIGRDPAVWEKPEEFMPERFMRD
                     GWDKSNSYSGQDFRYLPFGSGRRICPGANFGLATMEIMLANLMYHFDWEVPNEKEDGC
                     WKVSMDEKFGLMLRRNELLYLVPRASS"
     intron          2737. .2832
                     /gene="cyp71c3"
                     /number=1
     exon            2833. .3273
                     /gene="cyp71c3"
                     /number=2
     intron          3274. .3396
                     /gene="cyp71c3"
                     /number=2
     exon            3397. .>4029
                     /gene="cyp71c3"
                     /number=3
BASE COUNT     1263 a   1228 c   1270 g   1296 t
ORIGIN

  Query Match           1.5%;  Score 43;  DB 27;  Length 5057;
  Best Local Similarity  65.7%;  Pred. No. 8.02e-09;
  Matches    90;  Conservative    0;  Mismatches  47;  Indels   0;  Gaps   0;

Db     925 GATTCCTTCTATCGCGACGACTCGACCTATTGTGTTTTTATGTTGATTTGGACGATTTTC 984
           || || | |||||| |||||||  |   | | |   || || ||||||| ||   |||||
Cp    1353 gagtcttcctatcgtgacgacttaaagaaatatacattcatattgatttagatagttttc 1294
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Db    985 ACTAAAGCGATTCTCACGGAAGTGGGCTGAAAAGCTAAGCGTTTGGCAGTCCGCAACAGC 1044
          ||  ||  ||| |||||   || || |  |||| | |||| |||| | | |   ||| |
Cp   1293 acagaaatgatactcacatgagcggccaaaaaaacaaagcatttgactgccacaaactga 1234

Db   1045 TTCTGGTGGCCAGAATC 1061
          ||  | ||||||| ||||
Cp   1233 ttgcgatggccataatc 1217


RESULT   10
LOCUS       ZMA132240    6831 bp    DNA             PLN       15-JAN-1999
DEFINITION  Zea mays eIF-5 gene, exons 1-2.
ACCESSION   AJ132240
NID         g4160401
VERSION     AJ132240.1  GI:4160401
KEYWORDS    eIF-5 gene; eukaryotic translation initiation factor 5.
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
            Poaceae; Zea.
REFERENCE   1  (bases 1 to 6831)
  AUTHORS   Ignacio,L.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JAN-1999) Ignacio L.R., Genetica Molecular, Instituto
            de Biologia Molecular de Barcelona. CID. CSIC, C/ Jordi Girona
            Salgado 18-26, 08034 Barcelona, ESPANA
REFERENCE   2  (bases 1 to 6831)
  AUTHORS   Ignacio,L.R. and Pere,P.R.
  JOURNAL   Unpublished
COMMENT     Exist repetitive fragments to 1 from 1556 and  to 5357 from 5752.
FEATURES             Location/Qualifiers
     source          1. .6831
                     /organism="Zea mays"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /chromosome="4L"
     promoter        1556. .1901
                     /gene="eIF-5"
     gene            1556. .5162
                     /gene="eIF-5"
     TATA_signal     1645. .1651
                     /gene="eIF-5"
     TATA_signal     1665. .1670
                     /gene="eIF-5"
     TATA_signal     1822. .1828
                     /gene="eIF-5"
     exon            1902. .1949
                     /gene="eIF-5"
                     /number=1
     mRNA            join(1902. .1949,3248. .5162)
                     /gene="eIF-5"
     intron          1950. .3247
                     /gene="eIF-5"
                     /number=1
     exon            3248. .5162
                     /gene="eIF-5"
                     /number=2
     CDS             3545. .4900
                     /gene="eIF-5"
                     /codon_start=1
                     /product="eukaryotic translation initiation factor 5"
                     /protein_id="CAA10616.1"
                     /db_xref="PID:e1370838"
                     /db_xref="PID:g4160402"
                     /db_xref="GI:4160402"
                     /translation="MALQNIGASNRDDAFYRYKMPRMITKIEGRGNGIKTNVVNMVDI
                     AKALARPASYTTKYFGCELGAQSKFDEKTGISLVNGAHDTAKLAGLLEVFIKKYVQCY
                     GCGNPETEILISKTQMISLKCAACGFVSDVDMRDKLTTFILKNPPEQKKGGKDKKAMR
                     RAEKERLKEGEAADEEQKKLKKDAKKKGSKDSTAKGLKKKATTATGSDEDHSSSPTRS
                     HDGDKAAADDDDDDVQWQTDTSIEAAKQRMQEQLSAATAEMVMLSTEETEKKMKQPTH
                     KDGSTNGSAKEIPNDKPAVTKPSPYEELIGDIKASLGSAPTPSQLKAVLASSTLPPQD
                     VMNALLEALFGGVGKGFTKEVVKNKKYLAVAVPDEGAQTLLVQAIEAFGGKCNPEALK
                     EVPVVLKALYDGDILDEETIVDWYNDAVAAGKDSQVVKNAKPFVEWLQSAESDEEGDD
                     E"
     polyA_signal    4951. .4955
                     /gene="eIF-5"
     terminator      5138. .5142
                     /gene="eIF-5"
BASE COUNT     1867 a   1368 c   1490 g   2106 t
ORIGIN

  Query Match           1.5%;  Score 43;  DB 27;  Length 6831;
  Best Local Similarity  60.7%;  Pred. No. 8.02e-09;
  Matches   179;  Conservative    0;  Mismatches 112;  Indels   4;  Gaps   3;

Db    433 AGCTTCTGGCCACCAAAAGCTGCTGCGGACTGCCAAACGCTCAGCTTTTCAGCCAGCTTC 492
          || || |||||| |  || | | |   | | | |||| |||  | ||||  | | |||
Qy   1216 agattatggccatcgcaatcagtttgtggcagtcaaatgctttgttttttggccgctca 1275

Db    493 TATAAAATTCGTTAGGACAAAAACCATCTAAAATCAACATAAACACATAATCGGTTGAGT 552
          | | |   || ||      ||||| ||||||| |||| || ||   ||| |   || |||
Qy   1276 tgtgagtatcatttctgtgaaaactatctaaa-tcaatatgaatgtatatttctttaagt 1334

Db    553 CGTTGTAATAGTAGGAATCCGTCATTTTCTAGATCATGAGCACTATGAACAACTTTATCT 612
          |||    |||| | || ||| || ||  ||| | | | | |   |    ||| || ||||
Qy   1335 cgtcacgataggaagactccatcgtt--ctaaaacctaaaccatgcacacatattcatct 1392

Db    613 TCCTCCACACGTAATCGTAATGATACTCAAATTTTTCCCACAACCAGATTCTCCCCACAG 672
          | ||||| ||| ||   |  ||||| | | ||| |     || | ||||| ||   | |
Qy   1393 ttctccaaacgcaagtctcgtgatatttatattctcgtgccagctagattatctagaaat 1452

Db    673 CCAGATTTTCAGAAAAGCTGACCAGAAAAAAGCTGA-ACCAAACAGCCCCCATAGT 726
            ||||| | | ||||  |    |||||||| | | |||||||||  |||| ||
Qy   1453 ttagattcttaaaaaaattctttagaaaaaaaattatataccaaacaggaccatggt 1507


RESULT   11
LOCUS       AR024229      965 bp    DNA             PAT       04-DEC-1998
DEFINITION  Sequence 22 from patent US 5795961.
ACCESSION   AR024229
NID         g3977523
VERSION     AR024229.1  GI:3977523
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 965)
  AUTHORS   Wallace,T.Paul, Harris,W.J., Carr,F.J., Old,L.J., Welt,S. and
            Kitamura,K.
  TITLE     Recombinant human anti-Lewis b antibodies
  JOURNAL   Patent: US 5795961-A 22 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .965
                     /organism="unknown"
BASE COUNT      192 a    170 c    226 g    205 t    172 others
ORIGIN

  Query Match           1.4%;  Score 39;  DB 25;  Length 965;
  Best Local Similarity  16.8%;  Pred. No. 1.81e-06;
  Matches    18;  Conservative   56;  Mismatches  32;  Indels   1;  Gaps   1;

Db    843 RSSVTAADTAVYYCVRGRSYDSDGGDYWGGTTVTVSSHTVKDMTSSSSASVGDRVTTCRS 902
          :::: ||:||::: ::|: :: :  : : | |: :::: :::: ::  |:: :: |  ::
Qy   2714 acccgaaataatttcgggttttgcaagttgctacccgaaattc-ccaaacaaaattcggg 2772

Db    903 STTHGNGNTYYWYKGKAKYRVSNRSGVSRSGSGSGTDYTTSSDATYY 949
            ||:| |  :::::|: :::::  :|::     :  ::||::: |::
Qy   2773 tttcgggtatttcgggttcgggttcgggtattccaggtttgggtttc 2819


RESULT   12
LOCUS       MVU87256     1056 bp    DNA             MAM       02-JAN-1999
DEFINITION  Mustela vison GT dinucleotide repeat, chromosome 1q.
ACCESSION   U87256
```

```
NID         g4099442
VERSION     U87256.1  GI:4099442
KEYWORDS    .
SOURCE      American mink.
  ORGANISM  Mustela vison
            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Carnivora; Fissipedia; Mustelidae; Mustela.
REFERENCE   1  (bases 1 to 1056)
  AUTHORS   Brusgaard,K., Shukri,N.M., Malchenko,S., Koroleva,I. and Lohi,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-1997) Breeding and Genetics, Danish Institute of
            Animal Science, Blichersalle K25, Tjele 8830, DK
FEATURES             Location/Qualifiers
     source          1. .1056
                     /organism="Mustela vison"
                     /db_xref="taxon:9667"
                     /chromosome="1"
                     /map="1q"
                     /note="primers: 1167F: agcccctgcatatctacttctt, 1167R:
                     gaggatcttaccgctgttgag"
     primer_bind     98. .119
                     /standard_name="1167F"
     primer_bind     complement(300. .320)
                     /standard_name="1167R"
BASE COUNT      211 a    221 c    210 g    225 t    189 others
ORIGIN

  Query Match             1.3%;  Score 38;  DB 23;  Length 1056;
  Best Local Similarity  17.6%;  Pred. No. 6.78e-06;
  Matches    33;  Conservative   87;  Mismatches  64;  Indels   3;  Gaps   3;

Db     572 CCCWSCRHDVBMWSKWCWGKKSCCKSTGKDKMSGCAYCGKRMRRCSRYMMMRMCVGSGTW 631
           |||: |: :::: :::|   ::|| | :: ::|| :|  :::  :. :::::: :|   :
Qy    1070 cccaacagtccccttcccctccccatatt-acgcgtcaagcattgttcccaatcgtcct 1128

Db     632 ARCCCCDKKSGSGDKSHCKSKRKYKWMDRYHBCKSMCAMVRGKWSAGTGCMARGWRTWDS 691
             | |:::: :|::::| :: :: : : :::|:: | ::: :    || : :  : :::
Qy    1129 ctgcgcatgctggttcccacgtgtatttcctcgcgcgcagttctgttggaggaggaagg 1188

Db     692 SCTSTKGARRRKGMYARRKMYGTGAAWASAT-AYSTGAGTTBWRVTSWKMBKYKKTGMMH 750
           :  :  |  ::  ::|: :::|     |:|| |::    | : ::|::: ::::: |::
Qy    1189 cgggacgttggcactagcgctggctggagattatggccatcgcaatcag-tttgtggcag 1247

Db     751 HCAWKYG 757
           :||: :|
Qy    1248 tcaaatg 1254


RESULT   13
LOCUS       MZECPN60B    7905 bp    DNA             PLN       14-JUL-1993
DEFINITION  Corn nuclear-encoded mitochondrial chaperonin 60 (cpn60II) gene,
            complete cds.
ACCESSION   L21008
NID         g309558
VERSION     L21008.1  GI:309558
KEYWORDS    chaperonin 60; nuclear-encoded mitochondrial protein.
SOURCE      Zea mays (strain B73) (library: DashII of P.S.Close) DNA.
  ORGANISM  Zea mays
            Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
            Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
            Liliopsida; Poales; Poaceae; Zea.
REFERENCE   1  (bases 1 to 7905)
  AUTHORS   Close,P.S.
  TITLE     Molecular characterization of two nuclear genes encoding Zea mays
            mitochondrial chaperonin 60
  JOURNAL   Unpublished (1993)
FEATURES             Location/Qualifiers
     source          1. .7905
                     /organism="Zea mays"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /tissue_lib="DashII of P.S.Close"
                     /map="1L"
5'UTR       1711. .1913
                     /gene="cpn60II"
exon        1711. .1982
                     /gene="cpn60II"
                     /label=exon1
gene        join(1914. .1982,2409. .2540,2807. .2966,4035. .4210,
            4299. .4394,4698. .4802,4903. .4989,5080. .5169,5231. .5311,
            5397. .5465,5645. .5722,5816. .5911,6049. .6148,6309. .6412,
            6492. .6597,6700. .6778,7024. .7126)
                     /gene="cpn60II"
CDS         join(1914. .1982,2409. .2540,2807. .2966,4035. .4210,
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Db     337 TCGGGTAGAACGGGC-TACCCATACCCGAATCGAATTTTCTAGATACCCAAATTTTCAGG 395
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Cp    2476 tcgggtagtttgggaatacccgaacccgaacccgaaattccgggtacccgaaattccggg 2417

Db     396 TTTAGTTTAGATCGAGTACATTTTCGAGTATTATTTCTAAAAGCTCGAATTGTGAAAAGC 455
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Cp    2416 tattgaaaa-atccgttgtaatttcgggtattgattctcaaaacccgaaatttaaaaaac 2358

Db     456 CCAATCTAGCCGACCCAAAAAATACGGGCTAAATCAAATGCCCA 499
             |  || || |||| |||| | |||| |||  | || |||||
Cp    2357 ttgaattacccaacccgaaaatttcggg-taacccgaacgccca 2315


RESULT   14
LOCUS       AC005369    74371 bp    DNA             PRI       01-AUG-1998
DEFINITION  Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
            sequence.
ACCESSION   AC005369
NID         g3367505
VERSION     AC005369.1  GI:3367505
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 74371)
  AUTHORS   Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
  TITLE     Sequencing of human chromosome 5
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 74371)
  AUTHORS   Ricke,D.O.
  TITLE     Large Scale Sequence Analysis and Annotation with the Sequence
            Comparison Analysis (SCAN) System
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 74371)
  AUTHORS   Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome
            Institute, Lawrence Berkeley National Laboratory, MS 74-157,
            Berkeley, CA 94720, U.S.A.
COMMENT     Sequence submitted by:
            DOE Joint Genome Institute.
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     repeat_region   5327. .5602
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     repeat_region   6586. .6956
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     repeat_region   complement(7830. .8185)
                     /standard_name="possible repeat"
     repeat_region   8258. .8503
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     repeat_region   9070. .9387
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     repeat_region   complement(9740. .9845)
                     /rpt_family="MER42"
     repeat_region   complement(10440. .11015)
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     repeat_region   11950. .12250
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     repeat_region   12057. .12085
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     repeat_region   13727. .13750
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     repeat_region   14175. .14470
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     repeat_region   complement(17678. .18276)
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repeat_region   28987. .29214
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                40503. .40661,41868. .41972,42103. .42225,42492. .42569,
                44379. .44507))
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Qy   1008 gatatttggttagagcatcttcaagaaaacccgtaaatcaactccaaaaacgttttgagc 1067

Db  15900 TTTTTKWGASRSRGWSTCKCKCTSTSKCSCMSRSKSKRGWGYRSWKKYRCAMWMTCKSSK 15959
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Qy   1068 ctcccaacagtccccttcccctcccatattacgcgtcaagcattgttcccaatcgtc- 1126

Db  15960 CWCWSYRMRMKCYSCSYCYCSSGKKYWCRCSMYWYTCYYSYKYYWSMSYCTCTSWGWRWM 16019
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Db  16020 WSKGRSWMYASRSGCSCSCSMCMMCRCSCMSMKMWWWTTTTTKTRTWTTTWKWRKAGASA 16079
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Qy   1186 aggcgggacgttggcactagcgctggctggagattatggccatcgcaatcagttt-gtgg 1244

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RESULT   15
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DEFINITION  Sequence 5 from patent US 5569830.
ACCESSION   I28278
NID         g1819054
VERSION     I28278.1  GI:1819054
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 215)
  AUTHORS   Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
  TITLE     Plant inhibitors of fungal polygalacturonases and their use to
            control fungal disease
  JOURNAL   Patent: US 5569830-A 5 29-OCT-1996;
FEATURES             Location/Qualifiers
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